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      Cesson, Valerie
      Mach, Jean-Pierre
      Zauderer, Maurice
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Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Gly Gly Gly Ser Gly Thr 115 120 125

Gly Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr 130 135 140

Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly 145 150 155 160

Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu 165 170 175

Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg 180 185 190

Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser 195 200 205 Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu 210 215 220

Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly
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Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp 115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gly Gly Ser Gly Thr 130 135 140

Gly Gly Gly Ser Ala Arg Lys Cys Ser Leu Thr Gly Lys Trp Thr 145 150 155 160

Asn Asp Leu Gly Ser Asn Met Thr Ile Gly Ala Val Asn Ser Arg Gly 165 170 175

Glu Phe Thr Gly Thr Tyr Ile Thr Ala Val Thr Ala Thr Ser Asn Glu 180 185 190

Ile Lys Glu Ser Pro Leu His Gly Thr Gln Asn Thr Ile Asn Lys Arg 195 200 205

Thr Gln Pro Thr Phe Gly Phe Thr Val Asn Trp Lys Phe Ser Glu Ser 210 215 220

Thr Thr Val Phe Thr Gly Gln Cys Phe Ile Asp Arg Asn Gly Lys Glu 225 230 235 240

Val Leu Lys Thr Met Trp Leu Leu Arg Ser Ser Val Asn Asp Ile Gly 245 250 255

Asp Asp Trp Lys Ala Thr Arg Val Gly Ile Asn Ile Phe Thr Arg Leu 260 265 270

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Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 50 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp 115 120 125 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 130 135 140

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile 145 150 155 160

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu 165 170 175

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His 180 185 190

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg 195 200 205

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys 210 215 220

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu 225 230 235 240

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr 245 250 255

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu 260 265 270

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp 275 280 285

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val 290 295 300

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp 305 310 315 320

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His 325 330 335

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro 340 345 350

Gly Lys Gly Gly Gly Ser Gly Thr Gly Gly Gly Ser Ala Arg 355 360 365

Lys Cys Ser Leu Thr Gly Lys Trp Thr Asn Asp Leu Gly Ser Asn Met

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Thr	Val	Asn 435	Trp	Lys	Phe	Ser	Glu 440	Ser	Thr	Thr	Val	Phe 445	Thr	Gly	Gln	
Cys	Phe 450	Ile	Asp	Arg	Asn	Gly 455	Lys	Glu	Val	Leu	Lys 460	Thr	Met	Trp	Leu	
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978

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Ala As	sp (Glu	Thr 260	Trp	Tyr	Leu	Arg	Ala 265	Thr	Leu	Asp	Val	Val 270	Ala	Gly		
Glu Al		Ala 275	Gly	Leu	Ser	Cys	Arg 280	Val	Lys	His	Ser	Ser 285	Leu	Glu	Gly		
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accetectee aagageacet etgggggeae ageggeeetg ggetgeetgg teaaggaeta
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totottgtac tacactgaat toaccoccac tgaaaaagat gagtatgcot googtgtgaa
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Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Gly Gly Gly Ser Gly Thr 115 120 125

Gly Gly Gly Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser 130 135 140

Arg His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val 145 150 155 160

Ser Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly 165 170 175

Glu Arg Ile Glu Lys Val Glu His Ser Asp Leu Val Phe Ser Lys Asp 180 185 190

Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys
195 200 205

Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys 210 215 220

Ile Val Lys Trp Asp Arg Asp Met Thr Gly His His His His His 225 .230 .235 .240

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<211> 783

<212> DNA

<213> Artificial Sequence <220> Nucleotide sequence of the chimeric F(ab')2-beta2-microglobulin <223> <400> 33 qcqqccqcaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg 60 egegeatatg gteacegtet ceteageete caccaaggge ceateggtet teeceetgge 120 accetectee aagageaeet etgggggeae ageggeeetg ggetgeetgg teaaggaeta 180 cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240 cttcccggct gtcctacagt cctcaggact ctactccctc agcagcgtcg tgaccgtgcc 300 ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac 360 420 caaggtggac aagaaagttg agcccaaatc ttgtgacaaa actcacacat gcccaccgtg cccaggaggc ggtgggtcag gtaccggagg cggtgggtca atccagcgta ctccaaagat 480 tcaggtttac tcacgtcatc cagcagagaa tggaaagtca aatttcctga attgctatgt 540 gtctgggttt catccatccg acattgaagt tgacttactg aagaatggag agagaattga 600 aaaagtggag cattcagact tgtctttcag caaggactgg tctttctatc tcttgtacta 660 cactgaattc accccactg aaaagatgag tatgcctgcc gtgtgaacca tgtgactttg 720 tcacagccca agatagttaa gtgggatcga gacatgaccg gtcatcatca ccatcaccat 780 tga 783 <210> 34 <211> 256 <212> PRT <213> Artificial Sequence Nucleotide sequence of the chimeric F(ab')2-beta2-microglobulin <223> <400> 34 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val 20 25

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp 115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gly Gly Ser Gly Thr 130 135 140

Gly Gly Gly Ser Ile Gln Arg Thr Pro Lys Ile Gln Val Tyr Ser 145 150 155 160

Arg His Pro Ala Glu Asn Gly Lys Ser Asn Phe Leu Asn Cys Tyr Val 165 170 175

Ser Gly Phe His Pro Ser Asp Ile Glu Val Asp Leu Leu Lys Asn Gly 180 185 190

Glu Arg Ile Glu Lys Val Glu His Ser Asp Leu Val Phe Ser Lys Asp 195 200 205

Trp Ser Phe Tyr Leu Leu Tyr Tyr Thr Glu Phe Thr Pro Thr Glu Lys 210 215 220

Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln Pro Lys 225 230 235 240

Ile Val Lys Trp Asp Arg Asp Met Thr Gly His His His His His His 245 250 255

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<211> 1435

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of the chimeric full IgG1-beta2 microglobulin

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120

<400> 35

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accetectee aagageac	ct ctgggggcac	agcggccctg	ggctgcctgg	tcaaggacta	180
cttccccgaa ccggtgac	gg tgtcgtggaa	ctcaggcgcc	ctgaccagcg	gcgtgcacac	240
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caaggtggac aagaaagt	g agcccaaatc	ttgtgacaaa	actcacacat	gcccaccgtg	420
cccagcacct gaactcct	gg ggggaccgtc	agtcttcctc	ttccccccaa	aacccaagga	480
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caccccact gaaaaaga	g agtatgcctg	ccgtgtgaac	catgtgactt	tgtcacagcc	1380
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<212> PRT

<213> Artificial Sequence

<220>

<223> Nucleotide sequence of the chimeric full IgG1-beta2 microglobulin <400> 36

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Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp 115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 130 135 140

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile 145 150 155 160

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu 165 170 175

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His 180 185 190

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg 195 200 205

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys 210 215 220

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu 225 230 235 240

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr 245 250 255

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp 275 280 285

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val 290 295 300

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp 305 310 315 320

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His 325 330 335

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro 340 345 350

Gly Lys Gly Gly Gly Ser Gly Thr Gly Gly Gly Ser Ile Gln 355 360 365

Arg Thr Pro Lys Ile Gln Val Tyr Ser Arg His Pro Ala Glu Asn Gly 370 375 380

Lys Ser Asn Phe Leu Asn Cys Tyr Val Ser Gly Phe His Pro Ser Asp 385 390 395 400

Ile Glu Val Asp Leu Leu Lys Asn Gly Glu Arg Ile Glu Lys Val Glu
405 410 415

His Ser Asp Leu Val Phe Ser Lys Asp Trp Ser Phe Tyr Leu Leu Tyr 420 425 430

Tyr Thr Glu Phe Thr Pro Thr Glu Lys Asp Glu Tyr Ala Cys Arg Val 435 440 445

Asn His Val Thr Leu Ser Gln Pro Lys Ile Val Lys Trp Asp Arg Asp 450 455 460

Met Thr Gly His His His His His 465 470

<210> 37

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer El Sense

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<400> cagacco	38 jgtc	cagtagagga	cgatgtcctg				30					
	39 921 DNA Arti	ificial Sequ	ıence									
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aatagca	gct	ggacgcgcac	cgacggcttg	gcgtggctgg	gggagctgca	gacgcacagc	180					
tggagca	acg	actcggacac	cgtccgctct	ctgaagcctt	ggtcccaggg	cacgttcagc	240					
gaccago	agt	gggagacgct	gcagcatata	tttcgggttt	atcgaagcag	cttcaccagg	300					
gacgtga	agg	aattcgccaa	aatgctacgc	ttatcctatc	ccttggagct	ccaggtgtcc	360					
gctggct	gtg	aggtgcaccc	tgggaacgcc	tcaaataact	tcttccatgt	agcatttcaa	420					
ggaaaag	ata	tcctgagttt	ccaaggaact	tcttgggagc	caacccaaga	ggccccactt	480					
tgggtaa	act	tggccattca	agtgctcaac	caggacaagt	ggacgaggga	aacagtgcag	540					
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ggccgtc	tgc	tgctggtgtg	ccatgtctca	ggattctacc	caaagcctgt	atgggtgaag	720					
tggatgc	999	gtgagcagga	gcagcagggc	actcagccag	gggacatcct	gcccaatgct	780					
gacgaga	cat	ggtatctccg	agcaaccctg	gatgtggtgg	ctggggaggc	agctggcctg	840					
tcctgtc	9 99	tgaagcacag	cagtctagag	ggccaggaca	tcgtcctcta	ctggaccggt	900					
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<210> 40 <211> 303 <212> PRT

<213> Artificial Sequence

<220>

<223> Construct of extracellular domain of CD1d

<400> 40

Met Gly Cys Leu Leu Phe Leu Leu Leu Trp Ala Leu Leu Gln Ala Trp 1 5 10 15

Gly Ser Ala Glu Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln 20 25 30

Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala 35 40 45

Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp Thr 50 55 60

Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln 65 70 75 80

Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr 85 90 95

Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu 100 105 110

Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala Ser 115 120 125

Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe 130 135 140

Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val Asn 145 150 155 160

Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr Val 165 170 175

Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu Leu 180 185 190

Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp 195 200 205

Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Val Cys 210 215 220

His Va 225	al Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met Arg 230 235 240									
Gly Gl	u Gln Glu Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn 245 250 255									
Ala As	p Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala Gly 260 265 270									
Glu Al	a Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu Gly 275 280 285									
Gln As 29	sp Ile Val Leu Tyr Trp Thr Gly His His His His His His 0 295 300									
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<220> <223>	F(ab)-CD1d sense fragment									
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<212> DNA

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<223> F(ab')2-CD1d antisense fragment
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<211> 38
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<223> IgG1-CD1d sense fragment
<400> 45
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<211> 45
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<400> 46
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<210> 47
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<212> DNA
<213> Artificial Sequence
<220>
<223> Artificial sense primer to construct extracellular CD1d
<400> 47
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cggggtaccg gaggcggtgg gtcagtcccg caaaggcttt tc
<210> 48
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
<223> Artificial antisense primer to construct extracellular CD1d
<400> 48
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<223> Nucleotide sequence of the chimeric F(ab)-CDld product <400> gcggccgcaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg 60 egegeatatg gteacegtet ceteageete caceaaggge ceateggtet teeceetgge 120 accetectee aagageacet etgggggeac ageggeeetg ggetgeetgg teaaggaeta 180 cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240 cttcccggct gtcctacagt cctcaggact ctactccctc agcagcgtcg tgaccgtgcc 300 ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccagcaacac 360 caaggtggac aagaaaggag gcggtgggtc aggtaccgga ggcggtgggt cagtcccgca 420 aaggetttte ecceteeget geeteeagat etegteette geeaatagea getggaegeg 480 caccgacggc ttggcgtggc tgggggagct gcagacgcac agctggagca acgactcgga 540 caccgtccgc tctctgaagc cttggtccca gggcacgttc agcgaccagc agtgggagac 600 gctgcagcat atatttcggg tttatcgaag cagcttcacc agggacgtga aggaattcgc 660 caaaatgcta cgcttatcct atcccttgga gctccaggtg tccgctggct gtgaggtgca 720 ccctgggaac gcctcaaata acttcttcca tgtagcattt caaggaaaag atatcctgag 780 tttccaagga acttcttggg agccaaccca agaggcccca ctttgggtaa acttggccat 840 tcaagtgctc aaccaggaca agtggacgag ggaaacagtg cagtggctcc ttaatggcac 900 ctgcccccaa tttgtcagtg gcctccttga gtcagggaag tcggaactga agaagcaagt 960 gaagcccaag gcctqqctqt cccqtqqccc caqtcctqqc cctqqccqtc tqctqctqqt 1020 gtgccatgtc tcaggattct acccaaagcc tgtatgggtg aagtggatgc ggggtgagca 1080 ggagcagcag ggcactcagc caggggacat cctgcccaat gctgacgaga catggtatct 1140 1200 1260 cagcagtcta gagggccagg acatcgtcct ctactggacc ggtcatcatc accatcacca 1264 ttga

<210> 50

<211> 416

<212> PRT

<213> Artificial Sequence

<220>

<220>

<223> Polypeptide sequence of the chimeric F(ab)-CD1d product

<400> 50

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Phe	Pro	Leu 35	Ala	Pro	Ser	Ser	Lys 40	Ser	Thr	Ser	Gly	Gly 45	Thr	Ala	Ala
Leu	Gly 50	Cys	Leu	Val	Lys	Asp 55	Tyr	Phe	Pro	Glu	Pro 60	Val	Thr	Val	Ser
Trp 65	Asn	Ser	Gly	Ala	Leu 70	Thr	Ser	Gly	Val	His 75	Thr	Phe	Pro	Ala	Val 80
Leu	Gln	Ser	Ser	Gly 85	Leu	Tyr	Ser	Leu	Ser 90	Ser	Val	Val	Thr	Val 95	Pro
Ser	Ser	Ser	Leu 100	Gly	Thr	Gln	Thr	Tyr 105	Ile	Cys	Asn	Val	Asn 110	His	Lys
Pro	Ser	Asn 115	Thr	Lys	Val	Asp	Lys 120	Lys	Gly	Gly	Gly	Gly 125	Ser	Gly	Thr
Gly	Gly 130	Gly	Gly	Ser	Val	Pro 135	Gln	Arg	Leu	Phe	Pro 140	Leu	Arg	Суѕ	Leu
Gln 145	Ile	Ser	Ser	Phe	Ala 150	Asn	Ser	Ser	Trp	Thr 155	Arg	Thr	Asp	Gly	Leu 160
Ala	Trp	Leu	Gly	Glu 165	Leu	Gln	Thr	His	Ser 170	Trp	Ser	Asn	Asp	Ser 175	Asp
Thr	Val	Arg	Ser 180	Leu	Lys	Pro	Trp	Ser 185	Gln	Gly	Thr	Phe	Ser 190	Asp	Gln
Gln	Trp	Glu 195	Thr	Leu	Gln	His	Ile 200	Phe	Arg	Val	Tyr	Arg 205	Ser	Ser	Phe
Thr	Arg 210	Asp	Val	Lys	Glu	Phe 215	Ala	Lys	Met	Leu	Arg 220	Leu	Ser	Tyr	Pro
Leu 225	Glu	Leu	Gln	Val	Ser 230	Ala	Gly	Cys	Glu	Val 235	His	Pro	Gly	Asn	Ala 240
Ser	Asn	Asn	Phe	Phe 245	His	Val	Ala	Phe	Gln 250	Gly	Lys	Asp	Ile	Leu 255	Ser

Phe	Gln	Gly	Thr 260	Ser	Trp	Glu	Pro	Thr 265	Gln	Glu	Ala	Pro	Leu 270	Trp	Val		
Asn	Leu	Ala 275	Ile	Gln	Val	Leu	Asn 280	Gln	Asp	Lys	Trp	Thr 285	Arg	Glu	Thr		
Val	Gln 290	Trp	Leu	Leu	Asn	Gly 295	Thr	Cys	Pro	Gln	Phe 300	Val	Ser	Gly	Leu		
Leu 305	Glu	Ser	Gly	Lys	Ser 310	Glu	Leu	Lys	Lys	Gln 315	Val	Lys	Pro	Lys	Ala 320		
Trp	Leu	Ser	Arg	Gly 325	Pro	Ser	Pro	Gly	Pro 330	Gly	Arg	Leu	Leu	Leu 335	Val		
Cys	His	Val	Ser 340	Gly	Phe	Tyr	Pro	Lys 345	Pro	Val	Trp	Val	Lys 350	Trp	Met		
Arg	Gly	Glu 355	Gln	Glu	Gln	Gln	Gly 360	Thr	Gln	Pro	Gly	Asp 365	Ile	Leu	Pro		
Asn	Ala 370	Asp	Glu	Thr	Trp	Tyr 375	Leu	Arg	Ala	Thr	Leu 380	Asp	Val	Val	Ala		
Gly 385	Glu	Ala	Ala	Gly	Leu 390	Ser	Cys	Arg	Val	Lys 395	His	Ser	Ser	Leu	Glu 400		
Gly	Gln	Asp	Ile	Val 405	Leu	Tyr	Trp	Thr	Gly 410	His	His	His	His	His 415	His		
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acco	ctcct	cc a	agag	gcaco	et ct	9999	gcac	ago	ggco	ctg	ggct	gcct	gg t	caag	gacta	1	80
ctto	cccc	gaa c	cggt	gaco	gg tg	tcgt	ggaa	cto	aggo	gcc	ctga	ccaç	geg g	gcgtg	cacac	2	40
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<210> 52

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> Polypeptide sequence of the chimeric F(ab')2-CD1d product

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Ala His Met Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val 20 25 30

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp 115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gly Gly Ser Gly Thr 130 135 140

Gly Gly Gly Ser Val Pro Gln Arg Leu Phe Pro Leu Arg Cys Leu 145 150 155 160

Gln Ile Ser Ser Phe Ala Asn Ser Ser Trp Thr Arg Thr Asp Gly Leu 165 170 175

Ala Trp Leu Gly Glu Leu Gln Thr His Ser Trp Ser Asn Asp Ser Asp 180 185 190

Thr Val Arg Ser Leu Lys Pro Trp Ser Gln Gly Thr Phe Ser Asp Gln
195 200 205

Gln Trp Glu Thr Leu Gln His Ile Phe Arg Val Tyr Arg Ser Ser Phe 210 215 220

Thr Arg Asp Val Lys Glu Phe Ala Lys Met Leu Arg Leu Ser Tyr Pro 225 230 235 240

Leu Glu Leu Gln Val Ser Ala Gly Cys Glu Val His Pro Gly Asn Ala 245 250 255

Ser Asn Asn Phe Phe His Val Ala Phe Gln Gly Lys Asp Ile Leu Ser 260 265 270

Phe Gln Gly Thr Ser Trp Glu Pro Thr Gln Glu Ala Pro Leu Trp Val 275 280 285

Asn Leu Ala Ile Gln Val Leu Asn Gln Asp Lys Trp Thr Arg Glu Thr 290 295 300

Val Gln Trp Leu Leu Asn Gly Thr Cys Pro Gln Phe Val Ser Gly Leu

660

305 310 315 Leu Glu Ser Gly Lys Ser Glu Leu Lys Lys Gln Val Lys Pro Lys Ala Trp Leu Ser Arg Gly Pro Ser Pro Gly Pro Gly Arg Leu Leu Val 345 Cys His Val Ser Gly Phe Tyr Pro Lys Pro Val Trp Val Lys Trp Met 360 Arg Gly Glu Gln Glu Gln Gly Thr Gln Pro Gly Asp Ile Leu Pro 375 Asn Ala Asp Glu Thr Trp Tyr Leu Arg Ala Thr Leu Asp Val Val Ala 390 395 Gly Glu Ala Ala Gly Leu Ser Cys Arg Val Lys His Ser Ser Leu Glu 410 Gly Gln Asp Ile Val Leu Tyr Trp Thr Gly His His His His His His 425 <210> 53 <211> 1963 <212> DNA <213> Artificial Sequence <220> <223> Nucleotide sequence of the chimeric IgG1-CD1d product <400> gcggccgcaa accatgggat ggagctgtat catcctcttc ttggtagcaa cagctacagg 60 egegeatatg gteacegtet ceteageete caceaaggge ceateggtet teeceetgge 120 accetectee aagageacet etgggggeac ageggeeetg ggetgeetgg teaaggaeta 180 cttccccgaa ccggtgacgg tgtcgtggaa ctcaggcgcc ctgaccagcg gcgtgcacac 240 cttcccggct gtcctacagt cctcaggact ctactccctc agcagcgtcg tgaccgtgcc 300 ctccagcagc ttgggcaccc agacctacat ctgcaacgtg aatcacaagc ccaqcaacac 360 caaggtggac aagaaagttg agcccaaatc ttgtqacaaa actcacacat gcccaccgtg 420 cccagcacct gaactcctgg ggggaccgtc agtcttcctc ttccccccaa aacccaagga 480 caccctcatg atctcccgga cccctgaggt cacatgcgtg gtggtggacg tgagccacga 540 agaccetgag gteaagttea actggtaegt ggaeggegtg gaggtgeata atgeeaagae 600

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Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala 35 40 45

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser 50 55 60

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val 65 70 75 80

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro 85 90 95

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys 100 105 110

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp 115 120 125

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly 130 135 140

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile 145 150 155 160

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu 165 170 175

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His 180 185 190

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg 195 200 205

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys 210 215 220

Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu 225 230 235 240

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
245 250 255

Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu 260 265 270

- Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp 275 280 285
- Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val 290 295 300
- Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp 305 310 315 320
- Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 325 330 335
- Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro 340 345 350
- Gly Lys Gly Gly Gly Ser Gly Thr Gly Gly Gly Ser Val Pro 355 360 365
- Gln Arg Leu Phe Pro Leu Arg Cys Leu Gln Ile Ser Ser Phe Ala Asn 370 375 380
- Ser Ser Trp Thr Arg Thr Asp Gly Leu Ala Trp Leu Gly Glu Leu Gln 385 390 395 400
- Thr His Ser Trp Ser Asn Asp Ser Asp Thr Val Arg Ser Leu Lys Pro 405 410 415
- Trp Ser Gln Gly Thr Phe Ser Asp Gln Gln Trp Glu Thr Leu Gln His
 420 425 430
- Ile Phe Arg Val Tyr Arg Ser Ser Phe Thr Arg Asp Val Lys Glu Phe 435 440 445
- Ala Lys Met Leu Arg Leu Ser Tyr Pro Leu Glu Leu Gln Val Ser Ala 450 455 460
- Gly Cys Glu Val His Pro Gly Asn Ala Ser Asn Asn Phe Phe His Val 465 470 475 480
- Ala Phe Gln Gly Lys Asp Ile Leu Ser Phe Gln Gly Thr Ser Trp Glu 485 490 495
- Pro Thr Gln Glu Ala Pro Leu Trp Val Asn Leu Ala Ile Gln Val Leu
 500 505 510

Asn Gln Asp Lys Trp Thr Arg Glu Thr Val Gln Trp Leu Leu Asn Gly 515 520 525

Thr Cys Pro Gln Phe Val Ser Gly Leu Leu Glu Ser Gly Lys Ser Glu 530 535 540

Leu Lys Lys Gln Val Lys Pro Lys Ala Trp Leu Ser Arg Gly Pro Ser 545 550 555 560

Pro Gly Pro Gly Arg Leu Leu Val Cys His Val Ser Gly Phe Tyr . 565 570 575

Pro Lys Pro Val Trp Val Lys Trp Met Arg Gly Glu Gln Gln Gln 580 585 590

Gly Thr Gln Pro Gly Asp Ile Leu Pro Asn Ala Asp Glu Thr Trp Tyr 595 600 605

Leu Arg Ala Thr Leu Asp Val Val Ala Gly Glu Ala Ala Gly Leu Ser 610 615 620

Cys Arg Val Lys His Ser Ser Leu Glu Gly Gln Asp Ile Val Leu Tyr 625 630 635 640

Trp Thr Gly His His His His His 645